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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=2; day=19; hr=9; min=42; sec=47; ms=323; ]

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Reviewer Comments:

1.

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 11 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (11) POS (126)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 12 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (12) POS (0)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 12 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (12) POS (512)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 22 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (22) POS (112)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 24 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (24) POS (496)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 28 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (28) POS (16)

E355           Empty lines found between the amino acid numbering and the proteins SEQID ( 30 )

E321           No. of Bases conflict, this line has no nucleotides SEQID (30) POS (48)

<210> 11  
<211> 1582  
<212> DNA  
<213> Zea mays  
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<221> CDS  
<222> (10)..(1563)  
<223> Shrunken-2 gene revertant form  
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<221> variation  
<222> (267)  
<223> k = g or t; amino acid 86 = Ala.  
<220>  
<221> variation  
<222> (1368)  
<223> r = a or g; amino acid 453 = Pro.  
<220>  
<221> variation  
<222> (1578)  
<223> k = g or t.  
\* \* \* \* \*

gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc 387  
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe  
115 120 125

aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act 435  
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr

130 135 140

tcg ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac 483  
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Ile Asn  
145 150 155

For SEQ ID # 11, 12, 22, 24, 28, and 30 the sequence rules specify the numbering for amino acids be placed below the line of amino acids in a protein or coding region of a nucleotide sequence.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

(a) The symbols and format to be used for nucleotide and/or amino

acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

(d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

(4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID numbers listed above there are blank lines found between the amino acids and the numbering for the amino acids at different locations. Please remove all blank lines found between the amino acids and the numbering in these sequences.

2.

E300	Invalid codon found Asn SEQID (11) POS: 388
E300	Invalid codon found Ser SEQID (11) POS: 391
E300	Invalid codon found Gly SEQID (11) POS: 394
E300	Invalid codon found Ile SEQID (11) POS: 397
E300	Invalid codon found Asn SEQID (11) POS: 400
E300	Invalid codon found Lys SEQID (11) POS: 403
E300	Invalid codon found Ile SEQID (11) POS: 406
E300	Invalid codon found Phe SEQID (11) POS: 409
E300	Invalid codon found Val SEQID (11) POS: 412
E300	Invalid codon found Met SEQID (11) POS: 415
E300	Invalid codon found Ser SEQID (11) POS: 418
E300	Invalid codon found Gln SEQID (11) POS: 421
E300	Invalid codon found Phe SEQID (11) POS: 424
E300	Invalid codon found Asn SEQID (11) POS: 427
E300	Invalid codon found Ser SEQID (11) POS: 430
E300	Invalid codon found Thr SEQID (11) POS: 433

The errors shown above are ok and require no response.

\*\*\*\*\*

Application No: 10569000 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2010-02-18 13:09:42.494  
**Finished:** 2010-02-18 13:09:51.451  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 957 ms  
**Total Warnings:** 0  
**Total Errors:** 302  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 300	Invalid codon found Asn SEQID (11) POS: 388
E 300	Invalid codon found Ser SEQID (11) POS: 391
E 300	Invalid codon found Gly SEQID (11) POS: 394
E 300	Invalid codon found Ile SEQID (11) POS: 397
E 300	Invalid codon found Asn SEQID (11) POS: 400
E 300	Invalid codon found Lys SEQID (11) POS: 403
E 300	Invalid codon found Ile SEQID (11) POS: 406
E 300	Invalid codon found Phe SEQID (11) POS: 409
E 300	Invalid codon found Val SEQID (11) POS: 412
E 300	Invalid codon found Met SEQID (11) POS: 415
E 300	Invalid codon found Ser SEQID (11) POS: 418
E 300	Invalid codon found Gln SEQID (11) POS: 421
E 300	Invalid codon found Phe SEQID (11) POS: 424
E 300	Invalid codon found Asn SEQID (11) POS: 427
E 300	Invalid codon found Ser SEQID (11) POS: 430
E 300	Invalid codon found Thr SEQID (11) POS: 433
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)

**Input Set:**

**Output Set:**

**Started:** 2010-02-18 13:09:42.494  
**Finished:** 2010-02-18 13:09:51.451  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 957 ms  
**Total Warnings:** 0  
**Total Errors:** 302  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	This error has occurred more than 20 times, will not be displayed

**Input Set:**

**Output Set:**

**Started:** 2010-02-18 13:09:42.494  
**Finished:** 2010-02-18 13:09:51.451  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 957 ms  
**Total Warnings:** 0  
**Total Errors:** 302  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)

SEQUENCE LISTING

<110> University of Florida Research Foundation, Inc.  
Hannah, L. Curtis  
Lyerly Linebarger, Carla R.

<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase

<130> UF-371XC1 PCT

<140> 10569000  
<141> 2010-02-18

<150> US 60/496,188  
<151> 2003-08-18

<160> 42

<170> PatentIn version 3.2

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<212> DNA  
<213> zea mays

<400> 1

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caacataacct caatcctcaa	
gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag	180
attgtacc	
ttgacaaaaga agcgtgccaa gcctgcagtgc cattgggtg ccaactatag	240
actgattgat	
atccctgtca gcaattgtct caacagcaac atatccaaga tctatgtgct	300
aacgcaattt	
aactctgctt ccctaaccg tcacctctca agagcctacg ggagcaacat	360
tggagggtac	
aagaatgaag ggtttgtga agtcttagct gcacagcaga gccagataa	420
tccaaactgg	
tttcaaggta ctgcagatgc tgtaaggcag tacttgttg tggaggta	480
gcataatgtg	
atggaatttc taattcttgc tggcgatcac ctgtaccgg	540
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caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat	600
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cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat	660
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gagaaaccca aaggagagca gttgaaagca atgatggtg acaccaccat	720
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gatgacgtga gggcaaagga aatgccttat attgctagca tggtatcta	780
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gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct	900
gtatgatgg	
tactggaaag atatcggtac cattgcggca ttttataatg caaacttggg	960
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gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcataa aggtggaatt	1380
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 <213> zea mays

<400> 2

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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn			
20	25	30	

Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile			
35	40	45	

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys			
50	55	60	

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp			
65	70	75	80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val			
85	90	95	

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala			
100	105	110	

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val			
115	120	125	

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr			
130	135	140	

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val			
145	150	155	160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr			
165	170	175	

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val  
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met  
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys  
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu  
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
245 250 255

Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe  
260 265 270

Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr Ser  
275 280 285

Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp  
290 295 300

Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys  
305 310 315 320

Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile Tyr  
325 330 335

Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp Val  
340 345 350

Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys Ile  
355 360 365

Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala Ile  
370 375 380

Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu Ala  
385 390 395 400

Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile Gly  
405 410 415

Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg Ile  
420 425 430

Gly Asp Asn Val Lys Ile Leu Asn Ala Asp Asn Val Gln Glu Ala Ala  
435 440 445

Met Glu Thr Asp Gly Tyr Phe Ile Lys Gly Gly Ile Val Thr Val Ile  
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Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile  
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cgtgcaactg cattggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgc 660  
gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt 720  
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttagc 780  
aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaaagt 840  
gaggttattc caggtgcaac cagcatttggaa aagagggttc aggcttatct gtatgtgg 900  
tactggaaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag 960  
aagccaaatac cagatttcag cttctatgac cgttttgctc caatttatac acaacccgt 1020  
cacctgcccc cttcaaagggt tcttgatgtc gatgtgacag acagtgttat tggtaagga 1080  
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gataaaaaaac tccttgccga aaaagggtggc attcctattt gtttggaa aaattcatgc 1260  
atcaggagag caatcatttga caagaatgct cgaattggag acaatgtttaa gataactcaat 1320  
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gtcacagtga tcaaggatgc tttactccct agtgaaacag ttata 1425

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<211> 475

<212> PRT  
<213> zea mays

<400> 4

Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala  
1 5 10 15

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn  
20 25 30

Asp Ser Thr Cys Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile  
35 40 45

Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys  
50 55 60

Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp  
65 70 75 80

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val  
85 90 95

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala  
100 105 110

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val  
115 120 125

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr  
130 135 140

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val  
145 150 155 160

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr  
165 170 175

Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val  
180 185 190

Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met  
195 200 205

Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys  
210 215 220

Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu  
225 230 235 240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile  
245 250 255

Tyr	Val	Phe	Ser	Lys	Asp	Val	Met	Leu	Gln	Leu	Leu	Arg	Glu	Gln	Phe
							260		265				270		
Pro	Glu	Ala	Asn	Asp	Phe	Gly	Ser	Glu	Val	Ile	Pro	Gly	Ala	Thr	Ser
							275		280				285		
Ile	Gly	Lys	Arg	Val	Gln	Ala	Tyr	Leu	Tyr	Asp	Gly	Tyr	Trp	Glu	Asp
							290		295				300		
Ile	Gly	Thr	Ile	Ala	Ala	Phe	Tyr	Asn	Ala	Asn	Leu	Gly	Ile	Thr	Lys
							305		310				315		320
Lys	Pro	Ile	Pro	Asp	Phe	Ser	Phe	Tyr	Asp	Arg	Phe	Ala	Pro	Ile	Tyr
							325		330				335		
Thr	Gln	Pro	Arg	His	Leu	Pro	Pro	Ser	Lys	Val	Leu	Asp	Ala	Asp	Val
							340		345				350		
Thr	Asp	Ser	Val	Ile	Gly	Glu	Gly	Cys	Val	Ile	Lys	Asn	Cys	Lys	Ile
							355		360				365		
Asn	His	Ser	Val	Val	Gly	Leu	Arg	Ser	Cys	Ile	Ser	Glu	Gly	Ala	Ile
							370		375				380		
Ile	Glu	Asp	Ser	Leu	Leu	Met	Gly	Ala	Asp	Tyr	Tyr	Glu	Thr	Glu	Ala
							385		390				395		400
Asp	Lys	Lys	Leu	Leu	Ala	Glu	Lys	Gly	Gly	Ile	Pro	Ile	Gly	Ile	Gly
							405		410				415		
Lys	Asn	Ser	Cys	Ile	Arg	Arg	Ala	Ile	Ile	Asp	Lys	Asn	Ala	Arg	Ile
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Gly	Asp	Asn	Val	Lys	Ile	Leu	Asn	Ala	Asp	Asn	Val	Gln	Glu	Ala	Ala
							435		440				445		
Met	Glu	Thr	Asp	Gly	Tyr	Phe	Ile	Lys	Gly	Gly	Ile	Val	Thr	Val	Ile
							450		455				460		
Lys	Asp	Ala	Leu	Leu	Pro	Ser	Gly	Thr	Val	Ile					
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<213> zea mays

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caagctcatg	atagtgttct	tggaaatcatt	ctggggaggtg	gtgctgggac	tagattgtac	180
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cccttgacaa	agaaggcgtgc	caaggctgca	gtgccattgg	gtgccaacta	tagactgatt	240
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 1 5 10 15

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 20 25 30

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly

35

40

45

Ile Ile Leu Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys

50 55 60

Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile  
65 70 75 80

Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr  
85 90 95

Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg  
100 105 110

Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu  
115 120 125

Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly  
130 135 140

Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn  
145 150 155 160

Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp  
165 170 175

Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr  
180 185 190

Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu  
195 200 205

Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro  
210 215 220

Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly  
225 230 235 240

Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly  
245 250 255

Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln  
260 265 270

Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr  
275 280 285

Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu  
290 295 300

Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr  
305 310 315 320

Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile  
325 330 335

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp

340

345

350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys  
355 360 365

Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala  
370 375 380

Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu  
385 390 395 400

Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile  
405 410 415

Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg  
420